In the Claims

Please amend the claims as follows. Applicants present a full set of claims showing markups of the claims with insertions and deletions indicated by underlining and strikethrough text, respectively.

1. (Currently amended) An isolated nucleic acid molecule selected from the group consisting of

(a) a nucleic acid molecule which ~~hybridizes under highly stringent conditions to a molecule having a~~ comprises the nucleotide sequence set forth as SEQ ID NO:4 and which encodes SEQ ID NO:5, ~~wherein the isolated nucleic acid molecule codes for a LAGE-1 tumor associated polypeptide, and wherein the high stringency hybridization conditions are hybridization at 65°C in hybridization buffer (3.5 x SSC, 0.02% Ficoll, 0.02% polyvinyl pyrolidone, 0.02% Bovine Serum Albumin, 25mM NaH_2PO_4 (pH 7), 0.5% SDS, 2mM EDTA), wherein SSC is 0.15M sodium chloride/0.015M sodium citrate, pH 7; SDS is sodium dodecyl sulphate; and EDTA is ethylenediaminetetracetic acid, or hybridization at 65°C in 3.5X SSC, 1X Denhardt's, 0.5% SDS, EDTA (2 mM), Na_2PO_4 (25 mM) and salmon sperm DNA (100 µg/ml).~~

(b) nucleic acid molecules that differ from the nucleic acid molecules of (a) in codon sequence due to the degeneracy of the genetic code, and

(c) ~~complete~~ full-length complements of (a) and (b), wherein the isolated nucleic acid molecule excludes nucleic acid molecules having the nucleotide sequence of SEQ ID NO:8.

2. (Currently amended) The isolated nucleic acid molecule of claim 1, wherein the isolated nucleic acid molecule ~~comprises~~ consists of the nucleotide sequence of SEQ ID NO:4.

3. (Currently amended) The isolated nucleic acid molecule of claim ~~2~~ 1, wherein the isolated nucleic acid molecule comprises the coding region of the nucleotide sequence of SEQ ID NO:4.

4-6. (Canceled)

7. (Currently amended) An isolated nucleic acid molecule selected from the group consisting of:

(a) a unique fragment of nucleotides 1-993 of SEQ ID NO:4 between 15 and 992 nucleotides in length, and

(b) full-length complements of "(a)", wherein the unique fragment excludes nucleic acid molecules which consist only of fragments of SEQ ID NO:8, and wherein the unique fragment comprises at least 5 contiguous nucleotides of SEQ ID NO:4 that are not present in SEQ ID NO:8.

8-16. (Canceled)

17. (Previously presented) An expression vector comprising the isolated nucleic acid molecule of claim 1 operably linked to a promoter.

18. (Original) A host cell transformed or transfected with the expression vector of claim 17.

19. (Original) The host cell of claim 18, wherein the host cell expresses an HLA molecule.

20-37. (Canceled)

38. (Previously presented) A method for diagnosing cancer, comprising:

contacting a biological sample isolated from a subject with an agent that hybridizes under high stringency hybridization conditions to the isolated nucleic acid molecule of claim 1, wherein the high stringency conditions are hybridization at 65°C in hybridization buffer (3.5 x SSC, 0.02% Ficoll, 0.02% polyvinyl pyrolidone, 0.02% Bovine Serum Albumin, 25mM NaH_2PO_4 (pH 7), 0.5% SDS, 2mM EDTA), wherein SSC is 0.15M sodium chloride/0.015M sodium citrate, pH 7; SDS is sodium dodecyl sulphate; and EDTA is ethylenediaminetetracetic

acid; or hybridization at 58°C in hybridization buffer containing 10mM TRIS (pH8.8), 50mM KCl and 1.5mM $MgCl_2$, or hybridization at 65°C in 3.5X SSC, 1X Denhardt's, 0.5% SDS, EDTA (2 mM), Na_2PO_4 (25 mM) and salmon sperm DNA (100 µg/ml) and

determining expression of the nucleic acid molecule in the sample, wherein the expression of the nucleic acid molecule is diagnostic for the presence of cancer in the subject.

39-56. (Canceled)

57. (Previously presented) The method of claim 38, wherein the expression of the nucleic acid molecule in the sample is determined by determining the hybridization between the agent and the nucleic acid molecule.

58. (Previously presented) The method of claim 57, wherein the hybridization between the agent and the nucleic acid molecule is determined by nucleic acid amplification.

59. (Previously presented) The method of claim 58, wherein the nucleic acid amplification is reverse transcribed polymerase chain reaction (RT-PCR).

60-61. (Canceled)